

## SEARCH REQUEST FORM

Scientific and Technical Information Center

Requester's Full Name: DAVID GUZO Examiner #: 70677 Date: 7/27/04  
Art Unit: 1636 Phone Number: (571) 272-0767 Serial Number: 10/032585  
Mail Box and Bldg Room Location: RA: 2A79 Results Format Preferred (circle): PAPER DISK E-MAIL  
Mailbox: 2C70

If more than one search is submitted, please prioritize searches in order of need.

\*\*\*\*\*  
Please provide a detailed statement of the search topic, and describe as specifically as possible the subject matter to be searched, including the elected species or structures, keywords, synonyms, acronyms, and registry numbers, and combine with the concept or novelty of the invention. Define any terms that may have a special meaning. Give examples or relevant citations, authors, etc., if known. Please attach a copy of the cover sheet, pertinent claims, and abstract.

Title of Invention: \_\_\_\_\_

Inventors (please provide full names): \_\_\_\_\_

Earliest Priority Filing Date: \_\_\_\_\_

\*For Sequence Searches Only\* Please include all pertinent information (parent, child, divisional, or issued patent numbers) along with the appropriate serial number.

*Please run a regular + interference sequence search  
on SEQ ID NO: 4068 and 5068.*

*4068 NA 26  
5068 1 20*

*Thanks*

*04*

*Gu 2585  
7/28 3h*

\*\*\*\*\*  
STAFF USE ONLY

	Type of Search	Vendors and cost where applicable
Searcher: _____	NA Sequence (#) _____	STN _____
Searcher Phone #: _____	AA Sequence (#) _____	Dialog _____
Searcher Location: _____	Structure (#) _____	Questel/Orbit _____
Date Searcher Picked Up: _____	Bibliographic _____	Dr.Link _____
Date Completed: _____	Litigation _____	Lexis/Nexis _____
Searcher Prep & Review Time: _____	Fulltext _____	Sequence Systems _____
Clerical Prep Time: _____	Patent Family _____	WWW/Internet _____
Online Time: _____	Other _____	Other (specify): _____

Db	34539	ATTTCGATTTAGGCTTCGAAGCTATGAAACC-----TGGTATGAAAGAAAAGCTTACCG	34592
OY	566	GAGTGTGCTTGGATCTATTTTAAATCCCTGTGCATCAAGTTGGCAGTGGTTGGAAA	655
Db	34593	GTAATTACATATATATCTCTACTTCAATCTGTAAACCCCAAGTTATCTTGGGTGTGAAG	34652
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Db	34653	CTCATGGCAAAAGCTTCTCTCTCCATTTGGCCCTGAAGAGCACTTTAAGCTATATCA	34712
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OY	767	TGATTGCAAGTTCTGAGAAAGGCTCACTGATAAGTCGAAGCTGGTTAGAAACCCAG	826
Db	34773	TCACTGCACACTTTTGGCGTAAGTTAGTCCCAAGGTTGAGGAGAGTGTAGATGTCACT	34832
OY	827	TTGCTGCCACTATGAAACAAGTGTCTATTCACATTAATGGGTGTGTTTGAACCAAGTCA	886
Db	34833	TATACCTGTGGGATTTAAACCATCTCCAGCTTTGATGACTGGC-----CCCAAGC	34883
OY	887	TTGAAGGTCAACACACTTATGGTGGCCAAAGTTGAATAACAGAACTGCGGTTTCAAGATC	946
Db	34884	CTGAAGGCTTAACTCTCAGTTGGGTCAAGTACGGTTTGCACAAAGATTTATTCGGTGC	34943
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Db	34944	AAGTTGACAGAAAGGTCGTGGTGGTTTAACTTGAACGTGCTTGGACCCGGCTATTA	35003
OY	1007	CCATATATTTTTCGAGAAATGATC 1033	
Db	35004	CTCTCGCTTTAGCAGTGAATTCATC 35030	

RESULT 9				
NMC0M38				
LOCUS	NMC0M38	1453 bp	mRNA	linear
DEFINITION	N. crassa mRNA M0M38.			
ACCESSION	X56883			
VERSION	X56883.1	GI:3025		
KEYWORDS	outer membrane protein.			
SOURCE	<i>Neurospora crassa</i>			
ORGANISM	<i>Neurospora crassa</i>			
	Eukaryote; Fungi; Ascomycota; Pezizomycotina; Sordariomycetes; Sordariomycetidae; Sordariales; Sordariaceae; Neurospora. 1 (bases 1 to 1453) Kiebler,M., Pfalzer,R., Solner,T., Griffiths,G., Horstmann,H., Pfeiffer,N. and Neupert,W. Identification of a mitochondrial receptor complex required for recognition and membrane insertion of precursor proteins <i>Nature</i> 348 (6302), 610-616 (1990)			
TITLE	JOURNAL			
	MEDLINE	91066945		
REFERENCE	PUBMED	2174514		
AUTHORS	2	(Bases 1 to 1453)		
TITLE	Kiebler,M.			
JOURNAL	Direct Submissio:n			
	Submitted (26-JUN-1992) M. Kiebler, Institut f Physiologische			
FEATURES	Chemie, der LMU Muenchen, Goethe 53, 8 Muenchen 2, FRG			
Source	Location/Qualifiers			
	1..1453			

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ORIGIN

Query Match	11.4%;	Score 133.8;	DB 8;	Length 1453;
Best Local Similarity	51.8%;	Pred. No. 4.4e-20;		
Matches 443; Conservative	0;	Mismatches 382;	Indels 30;	Gaps 5;

OY	138	CGATGTTATATCACTATAACGACACCGTAATCAATTGGAGTTAACCAACCCGGGAC	197
Db	97	CGATGCCCTTCAACCCCTTTACAGAAAGAGAAACAGTTGGCTTTTCCAAACCCCGGAC	156
OY	198	AATTGAAACCTTGAAACAGAGAGTTGGCCCGATGTTGTTTGGGTCAATATTTCTTCAC	257
Db	157	GATGAGAACCATGCCCGGACAGTTCCAACCGATACCCTCCTACCAACTCAGATTCTC	216
OY	258	AGGCTTGAAGCTGATTTAAACAAAGCCTTTCCATGATGCCAGACATTCCAACATCCCA	317
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OY	318	CACCTTAAGTATGGATTCACAGTTTACAGACCTATGCTTTCAGTGCCTATATATGCAAC	377
Db	277	CCAGTTGCCATGSGG---CAGAGGTTGAACCTTATGCTTGTCTCTCTTACGGAAC	333
OY	378	CGATGATTAATTTCTTCAAGATTAACATTTGACAAATGATTTATCAATTTCTGGTAGAATCAA	437
Db	334	CAACCAAGATTTGGCTCAGGGTAACTCGAACAGAGGGGCGCTCTCGACAGATTTCAA	393
OY	438	TTAAGGATGGGACAAATTCACAACTTTCCAAAGTCACATTCAATTAECTATGACAAAC	497
Db	394	CTACAGATGGGGTGACAGGACCAATCACCAAGACGCAATTCGATTTGGTGGCGCCA---	450
OY	498	ATCCATATATCAATTAGAACAAAGATTATCAAGCTAATGATTTGTTCTTCAATGTCAAAC	557
Db	451	GGATATGGCCCAAGTTTAGCATGAACACCTTGGCGAGCATTCAGTGCCTCCCTCAAGGC	510
OY	558	TTTGAACCTTAATCTTTTATACAGTAATGAATTCAGTGAAGTTGTTGATCTATATTT	617
Db	511	CATCAACCC---CTCTTCTCTTGACGGCGGCTCTCACCGGATATCTTTGTCGGCACTACCT	567
OY	618	ACATTCCTTGTATCCACAGTTGGAGTGGAGTGGTGGAAACCATGATCTCCAAAGCAACAT	677
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OY	735	CGGCTCTGCTCACTCCCAAGTCAAGGTGCTTGTATGCAAGTTCTCGGAGAAAGTCAC	794
Db	688	TGCTAGGCTCAGTCTCCAGGCTCAGGGTGTCTCCACATCTCTCTCGGAGAAAGTCAC	747
OY	795	TGATTAAGTGGAAAGCTGGTTAGAAACCCAAAGTGTGTCACATATGAAACAAAGTGTGTA	854
Db	748	GGATAGGGTCAAGGCTGTGTGA-----TATGACGCTATCTGTTC	789
OY	855	TTCATTATAGGGGTGTGGTTTGAACCATGTCATTTGAAGTCAAACTATCTATTTGGTGC	914
Db	790	TTCCTCTCAAGAGCATGATGGGTGCTTACCAAGAGGATCACCACTTTTGGTGC	849
OY	915	GTATGATATCAGAACTCCGTTTTCAGAGTCAATGGATTTCAAAGGATGAAGTCAAGTGC	974
Db	850	GTAGACCTTCAAGATGTCACCTTTCAGGCTCAGATGATCTCCAAAGGCAAGCTCAAGTGC	909
OY	975	ATTTTTGAAGAAAGG	989

Db 910 CTTCGCTCAGAGACG 924

RESULT 10

CNS/IDNT 660 bp mRNA linear PLN 03-SEP-1999

LOCUS Botrytis cinerea strain T4 cDNA library under conditions of nitrogen deprivation.

DEFINITION

ACCESSION AL117029.1 GI:5832245

VERSION cDNA library; nitrogen deprivation.

KEYWORDS Botryotinia fuckeliana

SOURCE Botryotinia fuckeliana

ORGANISM Eukaryota; Fungi; Ascomycota; Pezizomycotina; Leotiomycetes; Helotiales; Sclerotiniaceae; Botryotinia.

REFERENCE 1 (bases 1 to 660)

AUTHORS Bitton, F., Lewis, C., Fortini, D., Pradier, J.M. and Brygoo, Y.

TITLE Direct Submission

JOURNAL Submitted (01-SEP-1999) Phytopathologie, INRA, route de St Cyr, 78028 Versailles, France

REFERENCE 2 (bases 1 to 660)

AUTHORS Genoscope.

TITLE Direct Submission

JOURNAL Submitted (01-SEP-1999) Genoscope - Centre National de Sequencage : CP 5706 91057 Evry cedex - FRANCE (E-mail : seqref@genoscope.cns.fr)

COMMENT - Web : www.genoscope.cns.fr

The cDNA library to be analyzed within the framework of this project was created using a Botrytis cinerea strain which was grown under conditions of nitrogen deprivation, which is the normal situation for B. cinerea during its development on its host plant. The library was produced in an oriented direction, in the pBSII vector.

FEATURES

source

1..660

location/Qualifiers

/organism="Botryotinia fuckeliana"

/mol\_type="mRNA"

/strain="T4"

/db\_xref="taxon:40559"

/note="Genoscope sequence ID : M40B11"

ORIGIN

Query Match 10.6%; Score 124.8; DB 8; Length 660;

Best Local Similarity 56.0%; Pvec. No. 5.7e-18;

Matches 344; Conservative 0; Mismatches 252; Indels 18; Gaps 5;

439 TACGATGGGACCAATTCACATTCACAGTCACTTACATTAAGCTCAGTACGACACCA 498

11 TACAGATGAGACTGCTGCTTGTACACAGCGAAGCTTCAAGTCCGCCCGGCA---A 67

499 TCCAGATGCCATTTGACACAGATTTAAAGCTAATGATTTCTTCAATCATGTCAAACT 558

68 GCTATGATGCAATTAAGACACGAGTAAACGACAAAGATTTCACAGCTTCAATCAATCT 127

559 TTGAACCTTAATTTTATCAGTAAATCAATCAAGTGAAGTGTGTTGATCTAATTTA 618

128 CTCACACCT---TCGATACCTGACGAGGATTAACCGTATTTTCATTTGGTCAATTTTA 184

619 CAATCTTGTATCCAAAGTGGCACTGGTTGGAACCAATGATCTCAACACCACTT- 677

185 CAAAGTGTGATCCAAACCTTGTCTTGGATTTGAGGTGTCTGGCAACGGCGACATG 244

678 --AGCACACACAGACAGCTGTTTCTATATGCTCTTATTAAGACGCAACTGGATC 735

245 AACCAAGAGCCGGAATCGCGGTATCATATGTGCAAAATACAGGATAGATGGAT 304

736 GCGTCTGCTCACTCCAGCTCAAGTTCATTTGATGAAATTTCTGAGAAAGTCACT 795

305 GCTAAGCTCATTTCAAGCGGAGAGAGCTTCAACATCGTTCTGAAAGATGACA 364

796 GATTAAGTGAAGCTGTTTGAACCAACCAAGTTCGCTCACTAAGAAACAAGTTGCTAT 855

365 GATAAGTCGAAGCTGCTGTGATCTTAATTCGCAATTCGAGGATGTCTGAGCTGG- 423

Db 856 CCATTAATGGGTGTGGTTTGAACACAGTCATGAAAGTCAAACTACTATTGGTGCCAG 915

424 --AATGATGGAGGCCCAATTAG-----MAGAGGCTGTCAACACTGTTGGCCAG 475

916 TAGAATACAGAACTGCCGTTTGAAGTCAATTTGATTCAAAGGATAGATCACTGCA 975

476 TATTAATTCAGAAATGTTACTTTCAGAGCCCAAGTATGATCAACCGAAAGTTGAGCTGC 535

976 TTTTGAAGAAAGAAATCAATGCAAGCTTTCATTTATTTCTGAGAAATTTGATCA 1035

536 TTATTAAGAAAGAAAGTGGCCCACTGTGCACTTACTTTTGGACCTGATGATCAT 595

1036 TTCAAGATTAATCATC 1049

596 TTCAAGCAGACGACG 609

RESULT 11

NCB10H4/C

LOCUS Neurospora crassa DNA linkage group V BAC contig B10H4.

DEFINITION

ACCESSION AL670010

VERSION AL670010.1 GI:18376274

KEYWORDS Neurospora crassa

SOURCE Neurospora crassa

ORGANISM Eukaryota; Fungi; Ascomycota; Pezizomycotina; Sordariomycetes; Eurotiomycetidae; Sordariaceae; Neurospora.

REFERENCE 1

AUTHORS Schulte, U., Aign, V., Hobeisel, J., Brandt, P., Fartmann, B., Holland, R., Nyakatura, G., Wewes, H.M. and Manhaupt, G.

TITLE Unpublished

JOURNAL 2 (bases 1 to 90763)

AUTHORS German Neurospora genome project.

TITLE Direct Submission

JOURNAL Submitted (18-JUN-2002) MIPS, Institut fuer Bioinformatik, GSF-Forschungszentrum fuer Umwelt und Gesundheit, GmbH, Ingolstaedter Landstrasse 11, D-85764 Neuberg, PFG, E-mail: G.Manhaupt@gsf.de Project Coordinator: Ulrich Schulte, Institute of Biochemistry, Heinrich-Heine-University, D-40225 Dueseldorf, E-mail: ulrich.schulte@uni-dueseldorf.de

This contig is an assembly of BAC 10H4 from 1 to: 70452, strain OR74A, and cosmid 6B10 from 70453 to: 90763, cosmid library pIOR1876xh, strain 74-OR-23-1A; BAC and cosmid clones are available at the Fungal Genetic Stock Center, <http://www.fgsc.net>

Sequencing was performed by MMD Biotech AG, Ebersberg, Germany, <http://www.mwgdna.com>

Information on performance of analysis and a more detailed annotation of this entry and other sequences of linkage groups II and V can be viewed at: <http://mbe.gsf.de/proj/neurospora>.

Location/Qualifiers

1..90763

/organism="Neurospora crassa"

/mol\_type="genomic DNA"

/db\_xref="taxon:5141"

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31067..35516

/gene="B10H4.010"

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/gene="B10H4.010"

/note="Similarity to cholesterol oxidase (EC 1.1.3.6) precursor, Streptomyces sp., PIR:A12260"

/codon\_start=1

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/protein\_id="CAD21388.1"

/db\_xref="GI:18376275"

/db\_xref="SPRMBL:08X08"

/translation="MDRLAHQNSNAPSPPTPACSGHLLGVKTDLAGLVGSHHTNG

COMMENT

Length 90763 bp DNA linear PLN 18-JUN-2002

Neurospora crassa DNA linkage group V BAC contig B10H4.

Neurospora crassa

Neurospora crassa

Eukaryota; Fungi; Ascomycota; Pezizomycotina; Sordariomycetes; Eurotiomycetidae; Sordariaceae; Neurospora.

Schulte, U., Aign, V., Hobeisel, J., Brandt, P., Fartmann, B., Holland, R., Nyakatura, G., Wewes, H.M. and Manhaupt, G.

Unpublished

2 (bases 1 to 90763)

German Neurospora genome project.

Direct Submission

Submitted (18-JUN-2002) MIPS, Institut fuer Bioinformatik, GSF-Forschungszentrum fuer Umwelt und Gesundheit, GmbH, Ingolstaedter Landstrasse 11, D-85764 Neuberg, PFG, E-mail: G.Manhaupt@gsf.de Project Coordinator: Ulrich Schulte, Institute of Biochemistry, Heinrich-Heine-University, D-40225 Dueseldorf, E-mail: ulrich.schulte@uni-dueseldorf.de

This contig is an assembly of BAC 10H4 from 1 to: 70452, strain OR74A, and cosmid 6B10 from 70453 to: 90763, cosmid library pIOR1876xh, strain 74-OR-23-1A; BAC and cosmid clones are available at the Fungal Genetic Stock Center, <http://www.fgsc.net>

Sequencing was performed by MMD Biotech AG, Ebersberg, Germany, <http://www.mwgdna.com>

Information on performance of analysis and a more detailed annotation of this entry and other sequences of linkage groups II and V can be viewed at: <http://mbe.gsf.de/proj/neurospora>.

Location/Qualifiers

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/organism="Neurospora crassa"

/mol\_type="genomic DNA"

/db\_xref="taxon:5141"

/chromosome="2"

1..34518

/note="Overlap to BAC contig J6F11, please refer to this entry for analysis and annotation"

31067..35516

/gene="B10H4.010"

join(31067..31724,31779..31895,31970..32537,32610..32947,33009..33198,33290..35516)

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/note="Similarity to cholesterol oxidase (EC 1.1.3.6) precursor, Streptomyces sp., PIR:A12260"

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/protein\_id="CAD21388.1"

/db\_xref="GI:18376275"

/db\_xref="SPRMBL:08X08"

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OY	661	TACTCCA	AGCA	CCAT	TTAG	CA	CCAA	CA	CA	AGCTGTTCT	TAT	720	
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OY	841	AAACA	AGTGC	TGAT	CCAT	TTAT	TGG	GTG	TTG	TAACCA	GTAT	900	
Db	913	AAACA	AGTGC	TGAT	CCAT	TTAT	TGG	GTG	TTG	TAACCA	GTAT	972	
OY	901	ACTAT	TG	TG	CCAT	TAT	GAAT	ATAC	AGAA	CTG	CCCTTT	960	
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Db	1033	GCTA	AGAT	CA	TG	CA	TTTTT	AGAAA	AGAA	AT	CA	1092	
OY	1021	GGAGAA	AT	TG	AT	CA	TTCA	TGA	AA	AT	CA	1080	
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Db	1153	GCTG	TA	TGA	AA	CA	AT	TG	TA	AT	CA	1212	
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Db	1213	ATCC	AG	TG	CTCC	AG	CTCC	AG	TG	CTTC	1243		

```

RESULT 8
US-10-603-113-3520
: Sequence 3520, Application US/10603113
: GENERAL INFORMATION:
: APPLICANT: Keith Weinstein et al
: TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO CANDIDA ALBICANS
: TITLE OF INVENTION: FOR DIAGNOSTICS AND THERAPEUTICS
: FILE REFERENCE: 107156.132
: CURRENT APPLICATION NUMBER: US/10/603.113
: CURRENT FILING DATE: 2003-06-24
: PRIOR APPLICATION NUMBER: US/03/248,796
: PRIOR FILING DATE: 1999-02-12
: NUMBER OF SEQ ID NOS: 26206
: SEQ ID NO 3520
: LENGTH: 1260
: TYPE: DNA
: ORGANISM: Candida albicans
US-10-603-113-3520

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Query Match	99.3%	Score 1164.6	DB 53	Length 1260
Best Local Similarity	99.7%	Pred. No. 1.3e-306		
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QY	1	ATGTCCTCAACAGATTAAATCCACCATTTGAGGCTCTACTAGACATAGCCAAAGTTGACATCCCA	60	
Dp	73	ATGTCCTCAACAGATTAAATCCACCATTTGAGGCTCTACTAGACATAGCCAAAGTTGACATCCCA	132	
QY	61	AGGTGGCTCTCAAGTGAACAACGGAACCAACAAAGCAAAATGATTTGGTGCATCAAAACCA	120	
Dp	133	AGGTGGCTCTCAAGTGAACAACGGAACCAACAAAGCAAAATGATTTGGTGCATCAAAACCA	192	
QY	121	GTTTTCAGTACATGAAGATGTTTATATATCACTTAAGAGAACCGTAAATCATTTGGGA	180	
Dp	193	GTTTTCAGTACATGAAGATGTTTATATCACTTAAGAGAACCGTAAATCATTTGGGA	252	
QY	181	TTAACCAACCCGGGAAACAATTGAAACCTTGAAACAAGAGGTTCCCGTGATGTTTTTG	240	
Dp	253	TTAACCAACCCGGGAAACAATTGAAACCTTGAAACAAGAGGTTCCCGTGATGTTTTTG	312	
QY	241	GGTCAATATTTCTTCAACAGGTTGAGAGCTGATTTAAACAAGCTTTTCAATGATGCCA	300	
Dp	313	GGTCAATATTTCTTCAACAGGTTGAGAGCTGATTTAAACAAGCTTTTCAATGATGCCA	372	
QY	301	GGATTCCAAAACATCCCAACATTTAAGATTTGATTCGAAGTTTATACAGCTATGCTTTC	360	
Dp	373	GGATTCCAAAACATCCCAACATTTAAGATTTGATTCGAAGTTTATACAGCTATGCTTTC	432	
QY	361	AGTGCCTTATAATGCCACCGATGATTATTTCTTCAAGATTAACATGACATGATTTATCA	420	
Dp	433	AGTGCCTTATAATGCCACCGATGATTATTTCTTCAAGATTAACATGACATGATTTATCA	492	
QY	421	TTTTCTGGTAGATCAATTAAGATGGGACAAATCAAACTTTCCAAAGTCACATTACA	480	
Dp	493	TTTTCTGGTAGATCAATTAAGATGGGACAAATCAAACTTTCCAAAGTCACATTACA	552	
QY	481	TTAGCTCATGGACAACATCCATGATGCCATTTGAAACAACAATTAATCAAGCTAATGATGT	540	
Dp	553	TTAGCTCATGGACAACATCCATGATGCCATTTGAAACAACAATTAATCAAGCTAATGATGT	612	
QY	541	TCATCAATGTCAAAACCTTGAAACCTTAACCTTTTATCAGTATGATTCAGTGGAGTT	600	
Dp	613	TCATCAATGTCAAAACCTTGAAACCTTTTATCAGTATGATTCAGTGGAGTT	672	
QY	601	GTGTTGGATCTATTTTACAATCTTGTGCATCCAAAGTGGCACTGGTTTGGAAACAG	660	
Dp	673	GTGTTGGATCTATTTTACAATCTTGTGCATCCAAAGTGGCACTGGTTTGGAAACAG	732	
QY	661	TACTCCAAACAACATTAGACACCAACAGACACAGCTGTTCTTAATGTTGGCTGTTTAAT	720	
Dp	733	TACTCCAAACAACATTAGACACCAACAGACACAGCTGTTCTTAATGTTGGCTGTTTAAT	792	
QY	721	GCAGCAACCTGAGATGCGCTCTGCTCAACTCCAAAGTCCAAAGTGCTTTGATTCGAAGTTTC	780	

DB 793 GAGGACACCTGATCCCTCTCTGCTCAACCTCAAGCTCAAGGTGCTTGAATTCAGGTTTC 852  
QY 781 TGGAGAAAGTCACTGATAAGAGCGAAGCGTTTGAAGAACCAAGTTGCTCCACTATG 840  
DB 853 TGGAGAAAGTCACTGATAAGAGCGAAGCGTTTGAAGAACCAAGTTGCTCCACTATG 912  
QY 841 AAACAAAGTCTGATCCATTAATGGGTGTGTTTGAACCAAGTCAATGAAGGTCAACT 900  
DB 913 AAACAAAGTCTGATCCATTAATGGGTGTGTTTGAACCAAGTCAATGAAGGTCAACT 972  
QY 901 ACTATGTCGCAAGATGAATGACAACTGCGCTTTGAGAGGTCAATGGAATCAAG 960  
DB 973 ACTATGTCGCAAGATGAATGACAACTGCGCTTTGAGAGGTCAATGGAATCAAG 1032  
QY 961 GGTAAATCATGCTATTTTGAAGAAAGATCATCCAACTGTTTCCATTAATTTTCT 1020  
DB 1033 GGTAAATCATGCTATTTTGAAGAAAGATCATCCAACTGTTTCCATTAATTTTCT 1092  
QY 1021 GGAAGAAATGATCAATTCAGATACATCTCGTTGGGTTTGGGTTTGAATTTGAGGT 1080  
DB 1093 GGAAGAAATGATCAATTCAGATACATCTCGTTGGGTTTGGGTTTGAATTTGAGGT 1152  
QY 1081 GCGGTATGATCAATTTGATGATGATGCAAGAGTTTGTGACAGCTGATGATGATCT 1140  
DB 1153 GCGGTATGATCAATTTGATGATGATGCAAGAGTTTGTGACAGCTGATGATGATCT 1212  
QY 1141 ATCCCAAGTCTCAAGCTCCAGGTGCTTGT 1171  
DB 1213 ATCCCAAGTCTCAAGCTCCAGGTGCTTGT 1243

RESULT 9  
US-60-096-409-3520  
Sequence 3520, Application US/60096409A

GENERAL INFORMATION:  
APPLICANT: Keitch Weinstock et al  
TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO CANDIDA ALBICAN  
FILE REFERENCE: GTC-016P  
CURRENT APPLICATION NUMBER: US/60/096,409A  
CURRENT FILING DATE: 1998-08-13  
NUMBER OF SEQ ID NOS: 28206  
SEQ ID NO 3520  
LENGTH: 1260  
TYPE: DNA  
ORGANISM: Candida albicans  
US-60-096-409-3520

Query Match 99.3%; Score 1164.6; DB 65; Length 1260;  
Best Local Similarity 99.7%; Pred. No. 1.3e-306;  
Matches 1167; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

QY 1 ATGTCTCAAGATTAATCAACCTTGGCTTACATGACATGACCAAGTTGACATCCCA 60  
DB 73 ATGTCTCAAGATTAATCAACCTTGGCTTACATGACATGACCAAGTTGACATCCCA 132  
QY 61 ACGTGGCTCAAGTGAACCAACCAACCAAGCAAGCAAGTGTGTCATCAAAACCA 120  
DB 133 ACGTGGCTCAAGTGAACCAACCAACCAAGCAAGTGTGTCATCAAAACCA 192  
QY 121 GTTTTCAGTTACATCAAGATGTTTATATCACTTAACCAACCAAGTGTGTCATCA 180  
DB 193 GTTTTCAGTTACATCAAGATGTTTATATCACTTAACCAACCAAGTGTGTCATCA 252  
QY 181 TTAAACCAACCGGGAACCAATGAAACCTGACAAAGAGTGGCCGTCATGTTTGG 240  
DB 253 TTAAACCAACCGGGAACCAATGAAACCTGACAAAGAGTGGCCGTCATGTTTGG 312  
QY 241 GGTCAATATTTCTTCAAGGTTGAGAGCTGATTTAAACCAAGCTTTTCCATGATCCA 300  
DB 313 GGTCAATATTTCTTCAAGGTTGAGAGCTGATTTAAACCAAGCTTTTCCATGATCCA 372

QY 301 GCATTCGAACATCCCACTTTAAGTATGATCCAAAGCTTTTACAGCTATGCTTTC 360  
DB 373 GCATTCGAACATCCCACTTTAAGTATGATCCAAAGCTTTTACAGCTATGCTTTC 432  
QY 361 AGTGCCTTATATGCAACCGATGATATTTCTTCAAGTATACATGACATGATTTATCA 420  
DB 433 AGTGCCTTATATGCAACCGATGATATTTCTTCAAGTATACATGACATGATTTATCA 492  
QY 421 TTTTCTGTAATCAATTCGATGGGACAAATCAACATTTCCAAAGTCAATTCACA 480  
DB 493 TTTTCTGTAATCAATTCGATGGGACAAATCAACATTTCCAAAGTCAATTCACA 552  
QY 481 TTAGCTGATGACCAACCATCATGATCATTTAGAACAGATTTATCAAGTATGATGT 540  
DB 553 TTAGCTGATGACCAACCATCATGATCATTTAGAACAGATTTATCAAGTATGATGT 612  
QY 541 TCTATCATGTCAAAATTTTGAACCTTAATTTTATCAGTATGATGATGATGATG 600  
DB 613 TCTATCATGTCAAAATTTTGAACCTTAATTTTATCAGTATGATGATGATGATG 672  
QY 601 GTTGTGATCTATTTTAAATCTGTCATCCAAAGTGGGAGTGGGTTTGAACCATG 660  
DB 673 GTTGTGATCTATTTTAAATCTGTCATCCAAAGTGGGAGTGGGTTTGAACCATG 732  
QY 661 TACTCCAAGAACCATTTAGCATCACAGACAGCTGTTTCTTATGTTGCTGATATAT 720  
DB 733 TACTCCAAGAACCATTTAGCATCACAGACAGCTGTTTCTTATGTTGCTGATATAT 792  
QY 721 GCAGGCAATGATGATGCTGCTGCTCACTCCAGCTCAAGTCTTGTGATGGAATTC 780  
DB 793 GCAGGCAATGATGATGCTGCTGCTCACTCCAGCTCAAGTCTTGTGATGGAATTC 852  
QY 781 TGAAGAAAGTCACTGATTAAGTGAAGTGTGTTGAACCAAGTGTGCTGCACTATG 840  
DB 853 TGAAGAAAGTCACTGATTAAGTGAAGTGTGTTGAACCAAGTGTGCTGCACTATG 912  
QY 841 AAACAAAGTGTGATTCATTAATGAGGTGTGTTTGAACCAAGTGTGCTGCACTATG 900  
DB 913 AAACAAAGTGTGATTCATTAATGAGGTGTGTTTGAACCAAGTGTGCTGCACTATG 972  
QY 901 ACTATGTCGCAAGATGAATGACAACTGCTTTCAGAGGTCAATGATGATCAAG 960  
DB 973 ACTATGTCGCAAGATGAATGACAACTGCTTTCAGAGGTCAATGATGATCAAG 1032  
QY 961 GGTAAATCATGCTATTTTGAAGAAAGATCATCCAACTGTTTCCATTAATTTTCT 1020  
DB 1033 GGTAAATCATGCTATTTTGAAGAAAGATCATCCAACTGTTTCCATTAATTTTCT 1092  
QY 1021 GGAAGAAATGATCAATTCAGATACATCTCGTTGGGTTTGGGTTTGAATTTGAGGT 1080  
DB 1093 GGAAGAAATGATCAATTCAGATACATCTCGTTGGGTTTGGGTTTGAATTTGAGGT 1152  
QY 1081 GCGGTATGATCAATTTGATGATGATGCAAGAGTTTGTGACAGCTGATGATGATCT 1140  
DB 1153 GCGGTATGATCAATTTGATGATGATGCAAGAGTTTGTGACAGCTGATGATGATCT 1212  
QY 1141 ATCCCAAGTCTCAAGCTCCAGGTGCTTGT 1171  
DB 1213 ATCCCAAGTCTCAAGCTCCAGGTGCTTGT 1243

RESULT 10  
US-10-326-956-3118  
Sequence 3118, Application US/10326956  
GENERAL INFORMATION:  
APPLICANT: Bauer et al  
TITLE OF INVENTION: Protein Complexes and Methods for their use  
FILE REFERENCE: 220615  
CURRENT APPLICATION NUMBER: US/10/326,956  
CURRENT FILING DATE: 2002-12-20  
PRIOR APPLICATION NUMBER: EP 01 130 253.6  
PRIOR FILING DATE: 2001-12-20  
NUMBER OF SEQ ID NOS: 3282